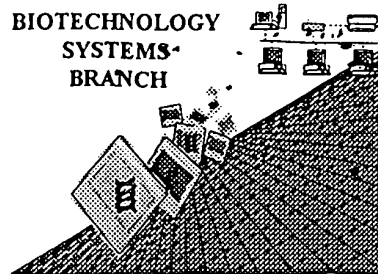


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/966 422

Source: OIE

Date Processed by STIC: 10/16/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/966422

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped.

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,422

DATE: 10/16/2001

TIME: 15:52:20

Input Set : A:\30534111.app

Output Set: N:\CRF3\10162001\I966422.raw

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202 tattaatgta cacattttat agatgaggaa aatgtggttc tgagaggtga agcattttgc 780
203 ctagtgatca cagctaaaaa gtgatagagc tgttctttat tttaaagttc acattgtact 840
204 accctggctc cctaatacaca gatgggcagg gtaggggttg ggtggggaca gaagttggag 900
205 agtggatgtg gctgccaaacc acacaagttg tgccaaccca cagattgagg aaagatgcta 960
206 aatttggaat ctggcaaaacc agtgtttggt tcttagctct gccacttcta agctgtgtga 1020
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208 attaaatgtg ataacacctg taaacatcta acagagtgcc tagcacatag cagggatcta 1140
209 gcaattgaat tagggttatt tgtttctgtc tactgattgg gtattgtttc tgacacttac 1200
210 ccaagtgtga atagcctata acactgggat aatttgtgaa atgatgctgc catctagtga 1260
211 aaaccaagac acacacacac acacacacac acacacacac acacacacac gtgcgcgcgc 1320
212 atggacaccc agcttcacca atgacaatat ggattggcat gttttagcct cacaacacag 1380
213 agccctgggg ctaactggca cctagagagg tcatctcggc cagtgccttc caaactacca 1440
214 gtgctgaaaa gccagttcaa aaaattttga acccattgca caccaatatt tttgtgaaat 1500
215 accataaaaa taaattactg gaaaaatgaa ataaaaata tgtataaaat acaaaccaaa 1560
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222 aggggttttt ttctggtttt taaaacaggt aaaggatgtc acagcaccac ttaataacat 1980
223 ttcttctgaa gtccagattt taacatctga tgccaataaa ttaactgctg agaacatcac 2040
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225 aaagaaagtt gccatagtaa cagtgaagtc actcctagat gccagtgaag atgcttttca 2160
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231 <212> TYPE: DNA

232 <213> ORGANISM: Homo sapiens

234 <220> FEATURE:

236 <400> SEQUENCE: 4

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239 aattagataa aacctgttgt ttattattat tcggcataat ggacttggtg gtttttctat 180
240 ttttcaatag atttgactt gaataagggtg aagaatttca cacaacatac aagagtacca 240
241 ttgttcctta tatcgttaaa tctttgtgac acactttgac aaaaatgtag aacctataac 300
242 aaattctttt acaagttact ataaaggaca caaagagaaa actttacctt ccagaacaaa 360
243 atgactcctg atgaacagtg tgtggggatt tgcttgatg tattaaactt ttgacctctg 420
244 aaaaaaaaaa aaaaaaaaaa aaaaaaaag 449

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247 <210> SEQ ID NO: 5

248 <211> LENGTH: 80

249 <212> TYPE: DNA

250 <213> ORGANISM: Artificial Sequence ✓

252 <220> FEATURE:

253 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓

254 oligos

256 <400> SEQUENCE: 5

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257 gctgtgcagc gctgagtgcg ttccaggtaa atgtcactaa cagaaaatag tgcagtaagg 60

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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,422

DATE: 10/16/2001

TIME: 15:52:20

Input Set : A:\30534111.app

Output Set: N:\CRF3\10162001\I966422.raw

3 <110> APPLICANT: Feder, J. N.
 4 Mintier, G.
 5 Ramanathan, C. S.
 6 Hawken, D. R.
 7 Cacace, A.
 8 Barber, L.
 9 Kornacker, M. G.
 11 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM6,
 12 EXPRESSED HIGHLY IN SMALL INTESTINE
 14 <130> FILE REFERENCE: D0040NP/3053-4119US3
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/966,422 of
 17 <141> CURRENT FILING DATE: 2001-09-26
 19 <150> PRIOR APPLICATION NUMBER: 60/235,602
 20 <151> PRIOR FILING DATE: 2000-09-27
 22 <150> PRIOR APPLICATION NUMBER: 60/306,604
 23 <151> PRIOR FILING DATE: 2001-07-19
 25 <150> PRIOR APPLICATION NUMBER: 60/315,412
 26 <151> PRIOR FILING DATE: 2001-08-28
 28 <160> NUMBER OF SEQ ID NOS: 81
 30 <170> SOFTWARE: PatentIn Ver. 2.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1683
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 37 <400> SEQUENCE: 1
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 40 cagaaaggag ctagcagttc tctagtcttc agttcaacat ttatacatat aaatgtggat 180
 41 ggccttaacc cagatgcaca gactgagctt caggtcttgc ttaatatgac gaaaaattac 240
 42 accaagacat gcggctttgt agtttatcaa aatgacaagc ttttccaate aaaaactttt 300
 43 acagctaaat cggattttag tcaaaaaatt atctcaagca aaactgatga aaatgagcaa 360
 44 gatcagagtg cttctgttga catggtcttt agtccaaagt acaacaaaaa agaatttcaa 420
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 46 tgtcaaaaag acaagggcac tgatggattc ctgcgctgcc gctgcaacca tactactaat 540
 47 tttgctgtat taatgacttt caaaaaggat tatcaaatat ccaaatcact tgacatatta 600
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 50 atgttgattt tcaacctcct ctttgtgttt ggaattgaaa actccaataa gaacttgacg 780
 51 acaagtgatg gtgacatcaa taatattgac ttgacaata atgacatacc caggacagac 840
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 53 ttagtgacat ttacctggaa cgcactcagc gctgcacagc tctattacct tctaataagg 960
 54 accatgaagc ctcttcctcg gcatttcatt cttttcatct cattaattgg atggggagtc 1020
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 59 ctgacaagca caaaaaagt ttcattccatg aagaagattg ttagcacatt atctgttgca 1320

Does Not Comply
Corrected Diskette Needed

Errored
 See Error Summary Sheet
 See page 6 of 7A

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,422

DATE: 10/16/2001

TIME: 15:52:20

Input Set : A:\30534111.app

Output Set: N:\CRF3\10162001\I966422.raw

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60 gttgtttttg gaattacctg gattctagca tacctgatgc tagttaatga tgatagcatc 1380
61 aggatcgtct tcagctacat attctgcctt ttcaacacta cacagggatt gcaaattttt 1440
62 atcctgtaca ctgttagaac aaaagtcttc cagagtgaag cttccaaagt gttgatgttg 1500
63 ctatcgtcta ttgggagaag gaagtcattg ccttcagtga cgcggccgag gctgcgtgta 1560
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66 tag 1683
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 560
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
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76 1 5 10 15
78 Asn Ile Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
79 20 25 30
81 Pro Ser Asn Val Arg Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu
82 35 40 45
84 Val Ser Ser Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro
85 50 55 60
87 Asp Ala Gln Thr Glu Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr
88 65 70 75 80
90 Thr Lys Thr Cys Gly Phe Val Val Tyr Gln Asn Asp Lys Leu Phe Gln
91 85 90 95
93 Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser
94 100 105 110
96 Ser Lys Thr Asp Glu Asn Glu Gln Asp Gln Ser Ala Ser Val Asp Met
97 115 120 125
99 Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu Phe Gln Leu Tyr Ser Tyr
100 130 135 140
102 Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
103 145 150 155 160
105 Cys Gln Lys Asp Lys Gly Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn
106 165 170 175
108 His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
109 180 185 190
111 Tyr Pro Lys Ser Leu Asp Ile Leu Ser Asn Val Gly Cys Ala Leu Ser
112 195 200 205
114 Val Thr Gly Leu Ala Leu Thr Val Ile Phe Gln Ile Val Thr Arg Lys
115 210 215 220
117 Val Arg Lys Thr Ser Val Thr Trp Val Leu Val Asn Leu Cys Ile Ser
118 225 230 235 240
120 Met Leu Ile Phe Asn Leu Leu Phe Val Phe Gly Ile Glu Asn Ser Asn
121 245 250 255
123 Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn Ile Asp Phe Asp
124 260 265 270
126 Asn Asn Asp Ile Pro Arg Thr Asp Thr Ile Asn Ile Pro Asn Pro Met
127 275 280 285
129 Cys Thr Ala Ile Ala Ala Leu Leu His Tyr Phe Leu Leu Val Thr Phe

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,422

DATE: 10/16/2001

TIME: 15:52:20

Input Set : A:\30534111.app

Output Set: N:\CRF3\10162001\I966422.raw

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258 cggcaatcgc agtgcacatg
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262 <211> LENGTH: 23
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
268 oligos
270 <400> SEQUENCE: 6
271 cagacacccat taacatcccg aat
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 22
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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283 <400> SEQUENCE: 7
284 agaatgaaat gccgaggaag ag
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288 <211> LENGTH: 1230
289 <212> TYPE: PRT
290 <213> ORGANISM: RAT
292 <400> SEQUENCE: 8
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294 1 5 10 15
296 Val His Ala Phe Ser Arg Ala Pro Ile Pro Met Ala Val Val Arg Arg
297 20 25 30
299 Glu Leu Ser Cys Glu Ser Tyr Pro Ile Glu Leu Arg Cys Pro Gly Thr
300 35 40 45
302 Asp Val Ile Met Ile Glu Ser Ala Asn Tyr Gly Arg Thr Asp Asp Lys
303 50 55 60
305 Ile Cys Asp Ser Asp Pro Ala Gln Met Glu Asn Ile Arg Cys Tyr Leu
306 65 70 75 80
308 Pro Asp Ala Tyr Lys Ile Met Ser Gln Arg Cys Asn Asn Arg Thr Gln
309 85 90 95
311 Cys Ala Val Val Ala Gly Pro Asp Val Phe Pro Asp Pro Cys Pro Gly
312 100 105 110
314 Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Glu Cys Val Pro Tyr Lys Val
315 115 120 125
317 Glu Gln Lys Val Phe Leu Cys Pro Gly Leu Leu Lys Gly Val Tyr Gln
318 130 135 140
320 Ser Glu His Leu Phe Glu Ser Asp His Gln Ser Gly Ala Trp Cys Lys
321 145 150 155 160
323 Asp Pro Leu Gln Ala Ser Asp Lys Ile Tyr Tyr Met Pro Trp Thr Pro
324 165 170 175
326 Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ser Ser Lys Asp Asp Phe Ile
327 180 185 190
329 Ala Gly Arg Pro Thr Thr Thr Tyr Lys Leu Pro His Arg Val Asp Gly

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VERIFICATION SUMMARY

DATE: 10/16/2001

PATENT APPLICATION: US/09/966,422

TIME: 15:52:21

Input Set : A:\30534111.app

Output Set: N:\CRF3\10162001\I966422.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1336 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1336 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: *Errored*
L:2066 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67
L:2066 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67
L:2066 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:2067 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67
L:2067 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67
L:2067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:2080 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68
L:2080 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68
L:2080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:2081 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68
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L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68

<210> 16
<211> 41
<212> PRT
<213> Artificial Sequence

<400> 16

Errored
Actual file contents
as of 11/02/01 met
12:07pm

A 213 response of "Artificial Sequence"
requires an explanation in Field 223.
MHA

FYI: Sequence 67 and Sequence 68
unknown must be represented in fields
221, 222 and 223 as
"unsure", location and possible values of
nucleotide residues.
MHA